

## SEQUENCE LISTING

<110> C. Frank Bennett  
Nicholas M. Dean  
Lex M. Cowser

<120> ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION

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Met Ala Cys Pro Trp Lys Phe Leu Phe
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Lys Thr Lys Phe His Gln Tyr Ala Met Asn Gly Glu Lys Asp Ile Asn
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Asn Asn Val Glu Lys Ala Pro Cys Ala Thr Ser Ser Pro Val Thr Gln
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Gln Pro Leu Val Glu Thr Gly Lys Lys Ser Pro Glu Ser Leu Val Lys
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715	720	725	
aag aac gtg ttc acc atg agg ctc aaa tct cgg cag aat cta caa agt			2441
Lys Asn Val Phe Thr Met Arg Leu Lys Ser Arg Gln Asn Leu Gln Ser			
730	735	740	745
ccg aca tcc agc cgt gcc acc atc ctg gtg gaa ctc tcc tgt gag gat			2489
Pro Thr Ser Ser Arg Ala Thr Ile Leu Val Glu Leu Ser Cys Glu Asp			
750	755	760	
ggc caa ggc ctg aac tac ctg ccg ggg gag cac ctt ggg gtt tgc cca			2537
Gly Gln Gly Leu Asn Tyr Leu Pro Gly Glu His Leu Gly Val Cys Pro			
765	770	775	
ggc aac cag ccg gcc ctg gtc caa ggc atc ctg gag cga gtg gtg gat			2585
Gly Asn Gln Pro Ala Leu Val Gln Gly Ile Leu Glu Arg Val Val Asp			
780	785	790	
ggc ccc aca ccc cac cag aca gtg cgc ctg gag gac ctg gat gag agt			2633
Gly Pro Thr Pro His Gln Thr Val Arg Leu Glu Asp Leu Asp Glu Ser			
795	800	805	
ggc agc tac tgg gtc agt gac aag agg ctg ccc ccc tgc tca ctc agc			2681
Gly Ser Tyr Trp Val Ser Asp Lys Arg Leu Pro Pro Cys Ser Leu Ser			
810	815	820	825
cag gcc ctc acc tac tcc ccg gac atc acc aca ccc cca acc cag ctg			2729
Gln Ala Leu Thr Tyr Ser Pro Asp Ile Thr Thr Pro Pro Thr Gln Leu			
830	835	840	
ctg ctc caa aag ctg gcc cag gtg gcc aca gaa gag cct gag aga cag			2777
Leu Leu Gln Lys Leu Ala Gln Val Ala Thr Glu Glu Pro Glu Arg Gln			
845	850	855	

860	865	870	
acc aac agc ccc aca ttc ctg gag gtg cta gag gag ttc ccg tcc ctg			2873
Thr Asn Ser Pro Thr Phe Leu Glu Val Leu Glu Glu Phe Pro Ser Leu			
875	880	885	
egg gtg tct gct ggc ttc ctg ctt tcc cag ctc ccc att ctg aag ccc			2921
Arg Val Ser Ala Gly Phe Leu Leu Ser Gln Leu Pro Ile Leu Lys Pro			
890	895	900	905
agg ttc tac tcc atc agc tcc tcc cgg gat cac acg ccc acg gag atc			2969
Arg Phe Tyr Ser Ile Ser Ser Ser Arg Asp His Thr Pro Thr Glu Ile			
910	915	920	
cac ctg act gtg gcc gtg gtc acc tac cac acc gga gat ggc cag ggt			3017
His Leu Thr Val Ala Val Val Thr Tyr His Thr Gly Asp Gly Gln Gly			
925	930	935	
ccc ctg cac cac ggt gtc tgc agc aca tgg ctc aac agc ctg aag ccc			3065
Pro Leu His His Gly Val Cys Ser Thr Trp Leu Asn Ser Leu Lys Pro			
940	945	950	
caa gac cca gtg ccc tgc ttt gtg cgg aat gcc agc gcc ttc cac ctc			3113
Gln Asp Pro Val Pro Cys Phe Val Arg Asn Ala Ser Ala Phe His Leu			
955	960	965	
ccc gag gat ccc tcc cat cct tgc atc ctc atc ggg cct ggc aca ggc			3161
Pro Glu Asp Pro Ser His Pro Cys Ile Leu Ile Gly Pro Gly Thr Gly			
970	975	980	985
atc gtg ccc ttc cgc agt ttc tgg cag caa cgg ctc cat gac tcc cag			3209
Ile Val Pro Phe Arg Ser Phe Trp Gln Gln Arg Leu His Asp Ser Gln			
990	995	1000	
cac aag gaa atg cgg gga ggc cgc atg acc ttg atg ttt ggg tgc cgc			3257
His Lys Gly Val Arg Gly Gly Arg Met Thr Leu Val Phe Gly Cys Arg			
1005	1010	1015	
cgc cca gat gag gac cac atc tac cag gag gag atg ctg gag atg gcc			3305
Arg Pro Asp Glu Asp His Ile Tyr Gln Glu Glu Met Leu Glu Met Ala			
1020	1025	1030	



1035	1040	1045	
ggc aag ccc aag gtc tat gtt cag gac atc ctg cgg cag cag ctg gcc			3401
Gly Lys Pro Lys Val Tyr Val Gln Asp Ile Leu Arg Gln Gln Leu Ala			
1050	1055	1060	1065
agc gag gtg ctc cgt gtg ctc cac aag gag cca ggc cac ctc tat gtt			3449
Ser Glu Val Leu Arg Val Leu His Lys Glu Pro Gly His Leu Tyr Val			
	1070	1075	1080
tgc ggg gat gtg cgc atg gcc cgg gac gtg gcc cac acc ctg aag cag			3497
Cys Gly Asp Val Arg Met Ala Arg Asp Val Ala His Thr Leu Lys Gln			
	1085	1090	1095
ctg gtg gct gcc aag ctg aaa ttg aat gag gag cag gtc gag gac tat			3545
Leu Val Ala Ala Lys Leu Lys Leu Asn Glu Glu Gln Val Glu Asp Tyr			
	1100	1105	1110
ttc ttt cag ctc aag agc cag aag cgc tat cac gaa gat atc ttc ggt			3593
Phe Phe Gln Leu Lys Ser Gln Lys Arg Tyr His Glu Asp Ile Phe Gly			
	1115	1120	1125
gct gta ttt cct tac gag gcg aag aag gac agg gtg gcg gtg cag ccc			3641
Ala Val Phe Pro Tyr Glu Ala Lys Lys Asp Arg Val Ala Val Gln Pro			
1130	1135	1140	1145
agc agc ctg gag atg tca gcg ctc tga gggcctacag gagggggttaa			3688
Ser Ser Leu Glu Met Ser Ala Leu			
	1150		
agctgccggc acagaactta aggatggagc cagctctgca ttatctgagg tcacagggcc			3748
tggggagatg gaggaaaagtg atateccccca acctcaagtc ttatttctctc aacgttgctc			3808
cgcataaaggc cetttaacttg acctcctaacc aagtagcacc ctgaatttat edgagacctcc			3868
tctctcaaac tggggcctcc ctggctccctt ggagacaaaa tetttaatgc caggcctggc			3928
gagtgggtga aagatggaac ttgctgctga gtgcaccact tcaagtgacc accaggaggt			3988
catgagctcatgcttgtgcttctctgagcctctgctgagcttatcttatcccctctgtatttta			4048

atggagatat ttacatgaat tgcattttac ttttaac

4145

&lt;210&gt; 11

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Primer

&lt;400&gt; 11

cgtccacagt atgtgaggat caa

23

&lt;210&gt; 12

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Primer

&lt;400&gt; 12

caagcaagac ttggacttgc aa

22

&lt;210&gt; 13

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Probe

&lt;400&gt; 13

tttcaccac aaggeccat cggatt

26

&lt;210&gt; 14

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

ggcacaattca acggcacagt

20

&lt;210&gt; 15

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Primer

&lt;400&gt; 15

gggtctcgct cctggaagct

20

&lt;210&gt; 16

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;223&gt; PCR Probe

&lt;400&gt; 16

aaggccgaga atgggaagct tgtcac

27

&lt;210&gt; 17

&lt;211&gt; 5484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (34)...(3960)

&lt;400&gt; 17

aartgtcagc acgggatctg agacttccaa aaa atg aag ccg gcg aca gga ctt  
Met Lys Pro Ala Thr Gly Leu

54

1

5

tag gtc tag gtc acc ctt ctc gtg gcg gcg ggg acc gtc cag ccc agc  
Trp Val Trp Val Ser Leu Leu Val Ala Ala Gly Thr Val Gln Pro Ser

102

Asp Ser Gln Ser Val Cys Ala Gly Thr Glu Asn Lys Leu Ser Ser Leu	
25 30 35	
tct gac ctg gaa cag cag tac cga gcc ttg cgc aag tac tat gaa aac	193
Ser Asp Leu Glu Gln Gln Tyr Arg Ala Leu Arg Lys Tyr Tyr Glu Asn	
40 45 50 55	
tgt gag gtt gtc atg ggc aac ctg gag ata acc agc att gag cac aac	246
Cys Glu Val Val Met Gly Asn Leu Glu Ile Thr Ser Ile Glu His Asn	
60 65 70	
cgg gac ctc tcc ttc ctg cgg tct gtt cga gaa gtc aca ggc tac gtg	294
Arg Asp Leu Ser Phe Leu Arg Ser Val Arg Glu Val Thr Gly Tyr Val	
75 80 85	
tta gtg gct ctt aat cag ttt cgt tac ctg cct ctg gag aat tta cgc	342
Leu Val Ala Leu Asn Gln Phe Arg Tyr Leu Pro Leu Glu Asn Leu Arg	
90 95 100	
att att cgt ggg aca aaa ctt tat gag gat cga tat gcc ttg gca ata	390
Ile Ile Arg Gly Thr Lys Leu Tyr Glu Asp Arg Tyr Ala Leu Ala Ile	
105 110 115	
ttt tta aac tac aga aaa gat gga aac ttt gga ctt caa gaa ctt gga	438
Phe Leu Asn Tyr Arg Lys Asp Gly Asn Phe Gly Leu Gln Glu Leu Gly	
120 125 130 135	
tta aag aac ttg aca gaa atc cta aat ggt gga gtc tat gta gac cag	486
Leu Lys Asn Leu Thr Glu Ile Leu Asn Gly Gly Val Tyr Val Asp Gln	
140 145 150	
aac aaa ttc ctt tgt tat gca gac acc att cat tgg caa gat att gtt	534
Asn Lys Phe Leu Cys Tyr Ala Asp Thr Ile His Trp Gln Asp Ile Val	
155 160 165	
cgg aac cca tgg cct tcc aac ttg act ctt gtg tca aca aat ggt act	582
Arg Asn Pro Trp Pro Ser Asn Leu Thr Leu Val Ser Thr Asn Gly Ser	
170 175 180	
tca gga tgt gga cgt tgc cat aag tcc tct act ggc cgt tgc tgg gga	630
Pro Gly Cys Gly Arg Cys His Lys Ser Cys Thr Gly Arg Cys Trp Gly	

Pro Thr Glu Asn His Cys Gln Thr Leu Thr Arg Thr Val Cys Ala Glu	
200	215
caa tgt gac ggc aga tgc tac gga cct tac gtc agt gac tgc tgc cat	726
Gln Cys Asp Gly Arg Cys Tyr Gly Pro Tyr Val Ser Asp Cys Cys His	
220	230
cga gaa tgt gct gga ggc tgc tca gga cct aag gac aca gac tgc ttt	774
Arg Glu Cys Ala Gly Gly Cys Ser Gly Pro Lys Asp Thr Asp Cys Phe	
235	245
gcc tgc atg aat ttc aat gac agt gga gca tgt gtt act cag tgt ccc	822
Ala Cys Met Asn Phe Asn Asp Ser Gly Ala Cys Val Thr Gln Cys Pro	
250	260
caa acc ttt gtc tac aat cca acc acc ttt caa ctg gag cac aat ttc	870
Gln Thr Phe Val Tyr Asn Pro Thr Thr Phe Gln Leu Glu His Asn Phe	
265	275
aat gca aag tac aca tat gga gca ttc tgt gtc aag aaa tgt cca cat	918
Asn Ala Lys Tyr Thr Tyr Gly Ala Phe Cys Val Lys Lys Cys Pro His	
280	295
aac ttt gtg gta gat tcc agt tct tgt gtg cgt gcc tgc cct agt tcc	966
Asn Phe Val Val Asp Ser Ser Ser Cys Val Arg Ala Cys Pro Ser Ser	
300	310
aag atg gaa gta gaa gaa aat ggg att aaa atg tgt aaa cct tgc act	1014
Lys Met Glu Val Glu Glu Asn Gly Ile Lys Met Cys Lys Pro Cys Thr	
315	325
gac att tgc cca aaa gct tgt gat ggc att ggc aca gga tca ttg atg	1062
Asp Ile Cys Pro Lys Ala Cys Asp Gly Ile Gly Thr Gly Ser Leu Met	
330	340
tca gct cag act gtg gat tcc agt aac att gac aaa ttc ata aac tct	1110
Ser Ala Gln Thr Val Asp Ser Ser Asn Ile Asp Lys Phe Ile Asn Cys	
345	355
acc aag atc aat ggg aat ttg atc ttt cta gtc act ggt att cat ggg	1158
Ala Thr Ile Asn Gly Asn Tyr Ile Phe Leu Val Thr Gly Ile His Gly	

Asp Pro Tyr Asn Ala Ile Glu Ala Ile Asp Pro Glu Lys Leu Asn Val	
380 385 390	
ttt cgg aca gtc aga gag ata aca ggt ttc ctg aac ata cag tca tgg	1254
Phe Arg Thr Val Arg Glu Ile Thr Gly Phe Leu Asn Ile Gln Ser Trp	
395 400 405	
cca cca aac atg act gac ttc agt gtt ttt tct aac ctg gtg acc att	1302
Pro Pro Asn Met Thr Asp Phe Ser Val Phe Ser Asn Leu Val Thr Ile	
410 415 420	
ggg gga aga gta ctc tat agt ggc ctg tcc ttg ctt atc ctc aag caa	1350
Gly Gly Arg Val Leu Tyr Ser Gly Leu Ser Leu Leu Ile Leu Lys Gln	
425 430 435	
cag ggc atc acc tct cta cag ttc cag tcc ctg aag gaa atc agc gca	1398
Gln Gly Ile Thr Ser Leu Gln Phe Gln Ser Leu Lys Glu Ile Ser Ala	
440 445 450 455	
gga aac atc tat att act gac aac agc aac ctg tgt tat tat cat acc	1446
Gly Asn Ile Tyr Ile Thr Asp Asn Ser Asn Leu Cys Tyr Tyr His Thr	
460 465 470	
att aac tgg aca aca ctc ttc agc aca atc aac cag aga ata gta atc	1494
Ile Asn Trp Thr Thr Leu Phe Ser Thr Ile Asn Gln Arg Ile Val Ile	
475 480 485	
cgg gac aac aga aaa gct gaa aat tgt act gct gaa gga atg gtg tgc	1542
Arg Asp Asn Arg Lys Ala Glu Asn Cys Thr Ala Glu Gly Met Val Cys	
490 495 500	
aac cat ctg tgt tcc agt gat ggc tgt tgg gga cct ggg cca gac caa	1590
Asn His Leu Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly Pro Asp Gln	
505 510 515	
tgt ctg tgg tgt cgc cgc ttc agt aga gga agg atc tgc ata gag tct	1638
Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys Ile Glu Ser	
520 525 530 535	
tgt aac ctc tat gat ggt gaa ttt cgg gag ttt gag aat ggc tcc atc	1686
Cys Asn Leu Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn Gly Ser Ile	

Cys Val Glu Cys Asp Pro Gln Cys Glu Lys Met Glu Asp Gly Leu Leu	
555	560
565	
aca tgc cat gga ccg ggt cct gac aac tgt aca aag tgc tct cat ttt	1782
Thr Cys His Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys Ser His Phe	
570	575
580	
aaa gat ggc cca aac tgt gtg gaa aaa tgt cca gat ggc tta cag ggg	1830
Lys Asp Gly Pro Asn Cys Val Glu Lys Cys Pro Asp Gly Leu Gln Gly	
585	590
595	
gca aac agt ttc att ttc aag tat gct gat cca gat cgg gag tgc cac	1878
Ala Asn Ser Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg Glu Cys His	
600	605
610	615
cca tgc cat cca aac tgc acc caa ggg tgt aac ggt ccc act agt cat	1926
Pro Cys His Pro Asn Cys Thr Gln Gly Cys Asn Gly Pro Thr Ser His	
620	625
630	
gac tgc att tac tac cca tgg acg ggc cat tcc act tta cca caa cat	1974
Asp Cys Ile Tyr Tyr Pro Trp Thr Gly His Ser Thr Leu Pro Gln His	
635	640
645	
gct aga act ccc ctg att gca gct gga gta att ggt ggg ctc ttc att	2022
Ala Arg Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile	
650	655
660	
ctg gtc att gtg ggt ctg aca ttt gct gtt tat gtt aga agg aag agc	2070
Leu Val Ile Val Gly Leu Thr Phe Ala Val Tyr Val Arg Arg Lys Ser	
665	670
675	
atc aaa aag aaa aga gcc ttg aga aga ttc ttg gaa aca gag ttg gtg	2118
Ile Lys Lys Lys Arg Ala Leu Arg Arg Phe Leu Glu Thr Glu Leu Val	
680	685
690	695
gaa cca tta act ccc agt ggc aca gca ccc aat caa gct caa ctt cgt	2166
Glu Pro Leu Thr Pro Ser Gly Thr Ala Pro Asn Gln Ala Gln Leu Arg	
700	705
710	
att ttg aaa gaa act gag ctg aag agg gta aaa gtc ctt ggc tca ggt	2214
Ala Thr Thr Thr Glu Thr Gly Leu Lys Arg Val Lys Val Leu Gly Ser Gly	

Ala Phe Gly Thr Val Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr	
730 735 740	
gtg aag att cct gtg gct att aag att ctt aat gag aca act ggt ccc	2310
Val Lys Ile Pro Val Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro	
745 750 755	
aag gca aat gtg gag ttc atg gat gaa gct ctg atc atg gca agt atg	2358
Lys Ala Asn Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met	
760 765 770 775	
gat cat cca cac cta gtc cgg ttg ctg ggt gtg tgt ctg agc cca acc	2406
Asp His Pro His Leu Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr	
780 785 790	
atc cag ctg gtt act caa ctt atg ccc cat ggc tgc ctg ttg gag tat	2454
Ile Gln Leu Val Thr Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr	
795 800 805	
gtc cac gag cac aag gat aac att gga tca caa ctg ctg ctt aac tgg	2502
Val His Glu His Lys Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp	
810 815 820	
tgt gtc cag ata gct aag gga atg atg tac ctg gaa gaa aga cga ctc	2550
Cys Val Gln Ile Ala Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu	
825 830 835	
gtt cat cgg gat ttg gca gcc cgt aat gtc tta gtg aaa tct cca aac	2598
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn	
840 845 850 855	
cat gtg aaa atc aca gat ttt ggg cta gcc aga ctc ttg gaa gga gat	2646
His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp	
860 865 870	
gaa aaa gag tac aat gct gat gga gga aag atg cca att aaa tgg atg	2694
Glu Lys Glu Tyr Asn Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met	
875 880 885	
gct ctg gag tgt ata cat tac agg aaa ttc acc cat cag agt gac gtt	2742
Val Thr Glu Gln Thr His Tyr Arg Lys Phe Thr His Gln Ser Asp Val	



Trp Ser Tyr Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys  
 905 910 915

ccc tat gat gga att cca acg cga gaa atc cct gat tta tta gag aaa 2838  
 Pro Tyr Asp Gly Ile Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu Lys  
 920 925 930 935

gga gaa cgt ttg cct cag cct ccc atc tgc act att gac gtt tac atg 2886  
 Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met  
 940 945 950

gtc atg gtc aaa tgt tgg atg att gat gct gac agt aga cct aaa ttt 2934  
 Val Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe  
 955 960 965

aag gaa ctg gct gct gag ttt tca agg atg gct cga gac cct caa aga 2982  
 Lys Glu Leu Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg  
 970 975 980

tac cta gtt att cag ggt gat gat cgt atg aag ctt ccc agt cca aat 3030  
 Tyr Leu Val Ile Gln Gly Asp Asp Arg Met Lys Leu Pro Ser Pro Asn  
 985 990 995

gac agc aag ttc ttt cag aat ctc ttg gat gaa gag gat ttg gaa gat 3078  
 Asp Ser Lys Phe Phe Gln Asn Leu Leu Asp Glu Glu Asp Leu Glu Asp  
 1000 1005 1010 1015

atg atg gat gct gag gag tac ttg gtc cct cag gct ttc aac atc cca 3126  
 Met Met Asp Ala Glu Glu Tyr Leu Val Pro Gln Ala Phe Asn Ile Pro  
 1020 1025 1030

cct ccc atc tat act tcc aga gca aga att gac tcg aat agg agt gaa 3174  
 Pro Pro Ile Tyr Thr Ser Arg Ala Arg Ile Asp Ser Asn Arg Ser Glu  
 1035 1040 1045

att gga cac agc cct cct cct gcc tac acc ccc atg tca gga aac cag 3222  
 Ile Gly His Ser Pro Pro Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln  
 1050 1055 1060

ttt gta tac cga gat gga ggt ttt gct gct gaa caa gga gtg tct gta 3270  
 Phe Val Tyr Arg Asp Gly Gly Phe Ala Ala Glu Gln Gly Val Ser Val

Pro Tyr Arg Ala Pro Thr Ser Thr Ile Pro Glu Ala Pro Val Ala Gln	
1080	1085 1090 1095
ggt gct act gct gag att ttt gat gac tcc tgc tgt aat ggc acc cta	3366
Gly Ala Thr Ala Glu Ile Phe Asp Asp Ser Cys Cys Asn Gly Thr Leu	
1100 1105 1110	
cgc aag cca gtg gca ccc cat gtc caa gag gac agt agc acc cag agg	3414
Arg Lys Pro Val Ala Pro His Val Gln Glu Asp Ser Ser Thr Gln Arg	
1115 1120 1125	
tac agt gct gac ccc acc gtg ttt gcc cca gaa cgg agc cca cga gga	3462
Tyr Ser Ala Asp Pro Thr Val Phe Ala Pro Glu Arg Ser Pro Arg Gly	
1130 1135 1140	
gag ctg gat gag gaa ggt tac atg act cct atg cga gac aaa ccc aaa	3510
Glu Leu Asp Glu Glu Gly Tyr Met Thr Pro Met Arg Asp Lys Pro Lys	
1145 1150 1155	
caa gaa tac ctg aat cca gtg gag gag aac cct ttt gtt tct cgg aga	3558
Gln Glu Tyr Leu Asn Pro Val Glu Glu Asn Pro Phe Val Ser Arg Arg	
1160 1165 1170 1175	
aaa aat gga gac ctt caa gca ttg gat aat ccc gaa tat cac aat gca	3606
Lys Asn Gly Asp Leu Gln Ala Leu Asp Asn Pro Glu Tyr His Asn Ala	
1180 1185 1190	
tcc aat ggt cca ccc aag gcc gag gat gag tat gtg aat gag cca ctg	3654
Ser Asn Gly Pro Pro Lys Ala Glu Asp Glu Tyr Val Asn Glu Pro Leu	
1195 1200 1205	
tac ctg aac acc ttt gcc aac acc ttg gga aaa gct gag tac ctg aag	3702
Tyr Leu Asn Thr Phe Ala Asn Thr Leu Gly Lys Ala Glu Tyr Leu Lys	
1210 1215 1220	
aac aac ata ctg tca atg cca gag aag gcc aag aaa ggc ttt gac aac	3750
Asn Asn Ile Leu Ser Met Pro Glu Lys Ala Lys Lys Ala Phe Asp Asn	
1225 1230 1235	
cct gac tac tgg aac cac agc ctg cca cct cgg agc acc ctt cag cac	3798
Pro Thr Thr Thr Ser His Ser Leu Pro Pro Arg Ser Thr Leu Gln His	

Pro Asp Tyr Leu Gln Glu Tyr Ser Thr Lys Tyr Phe Tyr Lys Gln Asn  
1260 1265 1270

ggg cgg atc cgg cct att gtg gca gag aat cct gaa tac ctc tct gag 3894  
Gly Arg Ile Arg Pro Ile Val Ala Glu Asn Pro Glu Tyr Leu Ser Glu  
1275 1280 1285

ttc tcc ctg aag cca ggc act gtg ctg ccg cct cca cct tac aga cac 3942  
Phe Ser Leu Lys Pro Gly Thr Val Leu Pro Pro Pro Tyr Arg His  
1290 1295 1300

cgg aat act gtg gtg taa gctcagttgt ggttttttag gtggagagac acacctgctc 4000  
Arg Asn Thr Val Val  
1305

caatttcccc accccctctt ctttctctgg tggctcttct tctaccccaa ggccagtagt 4060

tttgacactt cccagtggaa gatacagaga tgcaatgata gttatgtgct tacctaactt 4120

gaacattaga gggaaagact gaaagagaaa gataggagga accacaatgt ttcttcattt 4180

ctctgcatgg gttggtcagg agaataaaac agctagagaa ggaccagaaa atgtaaggca 4240

atgtgccta ctatcaaact agctgtcact ttttttcttt ttcttttctt ttctttgttt 4300

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ctgttcttat ctgcaggaac tgatgtgtgc atatttagca tccctggaaa tcataataaa 4420

gtttccatta gaacaaaaga ataacatttt ctataacata tgatagtgtc tgaaattgag 4480

aatccagttt ctttccccag cagtttctgt cctagcaagt aagaatggcc aactcaactt 4540

tcataattta aaaatctcca ttaaagttat aactagtaat tatgttttca acaatttttg 4600

gttttttca tttgttttg ctctgaccca ttcttttata ttgctcccc tatttttggc 4660

tttaatttct aattgcaaag atgtttacat caaagcttct tcacagaatt taagcaagaa 4720

atattttaat atagtgaat ggccactact ttaagtatc aatcttttaa ataagaaagg 4780

gggaaactaa gagacagttc tctgtgggtc aggaaaacta ctgatacttt caggggtggc 4960  
 ccaatgaggg aatccattga actggaagaa acacactgga ttgggtatgt ctacctggca 5020  
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